

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:21:33 ; Search time 11 Seconds
(without alignments)
20.462 Million cell updates/sec

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Listing first 45 summaries

Database : Published Applications AA:*

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SUMMARIES

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ALIGNMENTS

RESULT 1
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; Sequence 48620, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: Aenonica-X1
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/332,366
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2001-01-30
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 Patent No. US20020036598A1
 GENERAL INFORMATION:
 APPLICANT: Pravaga, Sudhirdas
 APPLICANT: Vernet, Corine
 APPLICANT: Shinkets, Richard A.
 APPLICANT: Burgess, Catherine
 APPLICANT: Spytek, Kimberly
 APPLICANT: Tcherniev, Velizar T.
 TITLE OF INVENTION: No. US20020036598A1 Polynucleotides and Polypeptides Encoded Th
 FILE REFERENCE: 15966-572 CIP1
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RESULT 3
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 Sequence 287, Application US/09992598
 Patent No. US20020160384A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
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 APPLICANT: Gurney, Austin L.
 APPLICANT: Klaavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoli, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tunas, Daniel
 APPLICANT: Watson, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William T.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C20
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.

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RESULT 4

US 09-999-293A-287

Sequence 287, Application US/09989293A

Patent No. US20020171764A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J.Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Klijavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Acids Encoding the Same Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C66

CURRENT APPLICATION NUMBER: US/09/989,293A

PRIOR APPLICATION NUMBER: 60/049787

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Query Match 52.2% Score 36; DB 9; Length 255;
 Best Local Similarity 71.4%; Pred. No. 1e+02; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

US-09-989-735-287
 Sequence 287, Application US/09989735
 Publication No. US20020193299A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J.Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kjelvin, Tvar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Ponzi, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE REFERENCE: P273OP1C61
 CURRENT APPLICATION NUMBER: US/09/9899,735
 CURRENT FILING DATE: 001-11-19
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PRIOR FILING DATE: 1998-07-09

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; Sequence 287, Application US/09990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:
; APPLICANT: Aszkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavim, Ivar J.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James
 APPLICANT: Peoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Wakabayashi, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2730P1C19

CURRENT APPLICATION NUMBER: US/A09/990,444

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 PRIOR FILING DATE: 1998-07-09

Query Match 52.4%; Score 36; DB 9; Length 255;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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 Db 42 YKKWENE 48

RESULT 7 US-09-989-722-287

Sequence 287 Application US/09989722
 Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
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 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P2730PIC63
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2% Score 36; DB 10; Length 25;
Best Local Similarity 71.4%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YKKWKN 9
Db 42 YKKWENE 48

RESULT 8
US 09-989-723-287
; Sequence
; Patent No. US 20020072092A1
; General Information:
; Applicant: Ashkenazi, Avi J.
; Applicant: Baker, Kevin P.
; Applicant: Borstein, David
; Applicant: Desnoyers, Luc
; Applicant: Eaton, Dan L.
; Applicant: Ferraro, Napoleone
; Applicant: Fong, Sherman
; Applicant: Gerber-Hanspeter
; Applicant: Gerritsen, Mary E.
; Applicant: Goddard, Audrey
; Applicant: Godowski, Paul J.
; Applicant: Grimaldi, J. Christopher
; Applicant: Gurney, Austin L.
; Applicant: Klijavin, Ivar J.
; Applicant: Napier, Mary A.
; Applicant: Pan, James
; Applicant: Paoni, Nicholas F.
; Applicant: Roy, Margaret Ann
; Applicant: Stewart, Timothy A.
; Applicant: Tumas, Daniel
; Applicant: Watanabe, Colin K.
; Applicant: Williams, P. Mickey
; Applicant: Wood, William T.
; Applicant: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC62
CURRENT APPLICATION NUMBER: US/09/989 723
CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/0493787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478

RESULT 10
05-09-989-727-287
; Sequence 287, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanae, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C65
; CURRENT APPLICATION NUMBER: US/09/989-727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/045787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YKKWKNK 9
Db 42 YKKWNE 48

RESULT 11

US-09-989-731-287
Sequence 287, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyer, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber-Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavim, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PICT0
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/09787
; PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182

RESULT 12
US-09-989-732-287
; Sequence 287, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Boisstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kjavian, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989, 732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/052250
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-06-03

Qy	3 YKKWKNK 9	Score 36;	DB 10;	Length 255;
	:	best local Similarity 71.4%;	Pred. No. 1e-02;	
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Db	42 YKKWNE 48		Gaps 0;	

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PRIOR APPLICATION NUMBER: 60/090429

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090697
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090698
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; Length 255;
Best local Similarity 71.4%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0;

Qy	3 YKKWNE 9
Db	42 YKKWNE 48

RESULT 15
US-09-991-163-287
; Sequence 287, Application US/09991163
; Patent No. US2002013223A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

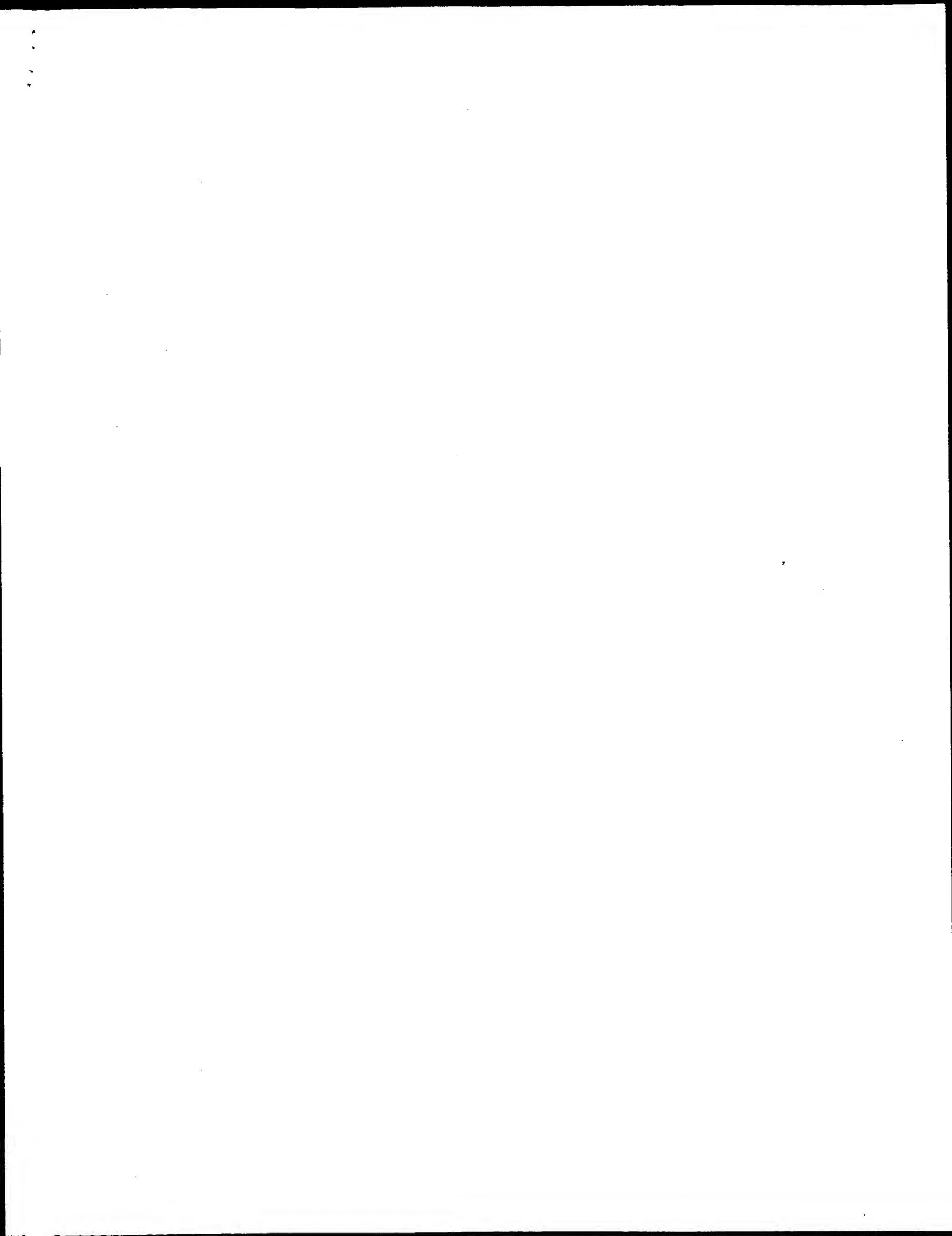

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PRIORITY APPLICATION NUMBER: 60/090694
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PRIORITY APPLICATION NUMBER: 60/091626
PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091633
PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091978
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/091982
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/092182
PRIORITY FILING DATE: 1998-07-09

Query Match          52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches      5; Conservative 2; Mismatches 0;
QY          3 YKKWKNK 9
Db          42 YKKWENE 48

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Search completed: December 30, 2002, 16:23:42
 Job time : 12 secs



Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on:

December 30, 2002, 16:18:08 ; Search time 35 Seconds

(without alignments)

4.9.493 Million cell updates/sec

Title: US-09-648-816B-9

Perfect score: 69

Sequence: 1 ALYKKWKNKLKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

908470 seqs, 133250620 residues

Post-processing: Minimum Match 0%

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8 Result No. Score Query Match Length DB ID

Result No.	Score	Query	Match Length	DB ID	Description
1	69	100.0	13	20	AY57471 Antimicrobial Pept
2	56	81.2	18	20	AY57472 Antimicrobial Pept
3	55	79.7	14	20	AY57470 Antimicrobial pept
4	53	76.8	18	20	AY57465 Antimicrobial Pept
5	53	76.8	19	20	AY57499 Antimicrobial pept
6	53	76.8	19	20	AY57501 Antimicrobial pept
7	53	76.8	20	20	AY57502 Antimicrobial Pept
8	53	76.8	25	20	AY57496 Antimicrobial Pept
9	53	76.8	35	20	AY57497 Antimicrobial Pept
10	49	71.0	18	20	AY57500 Antimicrobial Pept

ALIGNMENTS

RESULT 1

ID AAY57471
AAV57471 standard; Peptide: 13 AA.AC AAY57471;
XXDT 25-FEB-2000 (first entry)
XXDE Antimicrobial peptide RP-7 SEQ ID NO:9.
XXKW Antimicrobial; metopeptide; PMP-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.KW Synthetic.
OS Oryctolagus cuniculus.
XX

XX WO9942119-A1.

PD 26-AUG-1999.
XXPF 17-FEB-1999; 99W0-US03350.
XXPR 18-FEB-1998; 98US-0025319.
XXPA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XXPT Yeaman MR, Shen AJ;
XXDR WPI: 1999-527417/44.
XXPT Antimicrobial Peptides for potentiating antimicrobial agents active
against bacteria and fungi

PS Disclosure; Page 110; 166pp; English.
CC The present invention describes an antimicrobial peptide (AP) for direct CC activity or for potentiating antimicrobial agents active against CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide CC containing an amino acid sequence selected from the group consisting CC essentially of a first peptide template XZBZXBXB and its derivatives selected CC from XZBZXBXB, BXZXB, BXZXXB, XBZXXBX and BBXZBXZ; and CC (b) a second peptide template XBZXB and their derivatives selected from CC the group consisting of XBZXB, XBZXXBX, BXZXXB, XBZXXBX, and CC XBZXXBXZBX; where B = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY5763 to AAY5757 represent CC sequences used in the exemplification of the present invention.
XX SQ Sequence 13 AA;
Query Match 100.0%; Score 69; DB 20; Length 13; ID Best Local Similarity 100.0%; Pred. No. 0.00057; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 ALIKKKWNKLKS 13 Db 1 ALYKKWKNKLKS 13
RESULT 2
AY57472 ID AAY57472 standard; Peptide; 18 AA.
XX AC AAY57472;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-8 SEQ ID NO:10.
XX DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX KW synthetic.
OS OS Oryctolagus cuniculus.
XX PN WO942119-A1.
XX PD 26-AUG-1999.
XX PP 17-FEB-1999; 99WO-US03350.
XX PR 18-FEB-1998; 98US-6025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi -
XX Disclosure; Page 109; 166pp; English.
CC The present invention describes an antimicrobial peptide (AP) for direct CC activity or for potentiating antimicrobial agents active against CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide CC containing an amino acid sequence selected from the group consisting CC essentially of a first peptide template XZBZXBXB and its derivatives selected CC from XZBZXBXB, BXZXB, XBZXXBX and BBXZBXZ; and CC (b) a second peptide template XBZXB and their derivatives selected from CC the group consisting of XBZXB, XBZXXBX, XBZXXBX and BBXZBXZ; and CC XBZXXBXZBX; where B = at least one positively charged amino acid; CC Z = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY5763 to AAY5757 represent CC sequences used in the exemplification of the present invention.
XX SQ Sequence 18 AA;
Query Match 81.2%; Score 56; DB 20; Length 18; ID Best Local Similarity 83.3%; Pred. No. 0.068; Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0; QY 2 LYKKWNKLKS 13 Db 2 LYKKWKNKLKS 13
RESULT 3
AY57470 ID AAY57470 standard; Peptide; 14 AA.
XX AC AAY57470;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-6 SEQ ID NO:8.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
OS Oryctolagus cuniculus.
XX PN WO942119-A1.
XX PD 26-AUG-1999.
XX PP 17-FEB-1999; 99WO-US03350.
XX PR 18-FEB-1998; 98US-6025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi -
XX Disclosure; Page 109; 166pp; English.
CC The present invention describes an antimicrobial peptide (AP) for direct CC activity or for potentiating antimicrobial agents active against CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide CC containing an amino acid sequence selected from the group consisting CC essentially of a first peptide template XZBZXBXB and its derivatives selected CC from XZBZXBXB, BXZXB, XBZXXBX and BBXZBXZ; and CC (b) a second peptide template XBZXB and their derivatives selected from CC the group consisting of XBZXB, XBZXXBX, XBZXXBX and BBXZBXZ; and CC XBZXXBXZBX; where B = at least one positively charged amino acid; CC Z = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY5763 to AAY5757 represent CC sequences used in the exemplification of the present invention.
XX SQ Sequence 14 AA;

KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 Oryctolagus cuniculus.
 XX
 PN WO942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1999; 98US-0025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi -
 XX
 PS Disclosure; Page 59; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZXBKB and its derivatives
 CC selected from XBZBZXBKB, BXZXB, BXZXBZ, XBZXBKB and BBZBXZ; and
 CC (b) a second peptide template XBXX and their derivatives selected from
 CC the group consisting of XBXBKB, XBXXKB, XBXXBKB, BXBXKB, XBZXXB,
 CC XBZXBZBX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apperosis of microbial cells. AAY57463 to AAY5557 represent
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 19 AA:
 Query Match 76.8%; Score 53; DB 20; Length 19;
 Best Local Similarity 84.6%; Pred. No. 0.2;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKKWKNLKLS 13
 Db 1 ALYKKFKKKLKS 13
 XX
 SQ Sequence 19 AA:
 RESULT 7
 AAY57502
 ID AAY57502 standard; Peptide; 20 AA.
 XX
 AC AAY57502;
 XX
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 Oryctolagus cuniculus.
 XX
 PN WO942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1999; 98US-0025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi -
 XX Disclosure; Page 126; 16pp; English.
 CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXXB and its derivatives selected from XZBZBXXB, BZXB, BXZXB, XBZBXB and BBZBXZ; and (b) a second peptide template XBZB, BXZXB, XBZBXB and BBZBXZ; and the group consisting of XBZBXXB, XBZBXB, BXZXB, and XBZBXXBZB; where B = at least one non-polar hydrophobic amino acid; X = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY5463 to AAY5575 represent sequences used in the exemplification of the present invention.
 CC
 XX SQ Sequence 25 AA:
 Query Match Best Local Similarity Score DB 20; Length 25;
 Matches 11; Conservative Pred. No. 0.27; Mismatches 1; Indels 0; Gaps 0
 QY 1 ALYKKWKKLKS 13
 YY ||||| : | |||||
 Db 1 ALYKKFKKLKS 13
 AC AAY57497;
 XX DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
 KW Antimicrobial; metapptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 OS Oryctolagus cuniculus.
 XX PN WO9942119-R1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US03350.
 XX PR 18-FEB-1998; 98US-0025319.
 XX (HARB-) HARBOR-UCIA RES & EDUCATION INST.
 PI Yeaman MR, Shen AJ;
 XX DR WPI; 1999-527417/44.
 XX PP Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi -
 PT Disclosure; Page 126; 16pp; English.
 CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXXB and its derivatives selected from XZBZBXXB, BZXB, BXZXB, XBZBXB and BBZBXZ; and

CC sequences used in the exemplification of the present invention.

XX

SQ sequence 18 AA;

Query Match 71.0%; Score 49; DB 20; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.75; 1; Mismatches 10; Conservative 1; Indels 0; Gaps 0;

OY 1 ALYKKWKNKLK 12
Db 1 ALYKKFKKKLKLK 12

RESULT 11
AY57504 standard; Peptide; 18 AA.

XX

AC AAY57504;
XX
DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-1-10F SEQ ID NO:42.

XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX
OS Synthetic.
OS Oryctolagus cuniculus.

XX
PN WO9942119-A1.

XX
PD 26-AUG-1999.

XX
PF 17-FEB-1999; 99WO-US03350.

XX
PR 18-FEB-1998; 98US-0025319.

XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX
PI Yeaman MR, Shen AJ;

XX
DR WO9942119-A1.

XX
PR 18-FEB-1998; 99WO-US03350.

XX
PT 17-FEB-1999; 99WO-US03350.

XX
PR 18-FEB-1998; 98US-0025319.

XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX
PI Yeaman MR, Shen AJ;

XX
PR WO9942119-A1.

XX
PS Disclosure; Page 108; 166pp; English.

XX
PS The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBBZBXB and its derivatives selected from XBBZBXBX, BXBXB, BXZBXB, XBBXBXBX and BBZBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXB, XBBXXBX, BXBBX, XBBZXB, and XBBZBXBXZBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AY57463 to AY57557 represent sequences used in the exemplification of the present invention.

XX
SQ Sequence 13 AA;

Query Match 69.6%; Score 48; DB 20; Length 13;
Best Local Similarity 69.2%; Pred. No. 0.77; 1; Mismatches 9; Conservative 3; Indels 0; Gaps 0;

OY 1 ALYKKWKNKLKS 13
Db 1 ARYRKFKNKLKS 13

RESULT 13
AY57467 standard; Peptide; 14 AA.

XX
AC AAY57467;
XX
DT 25-FEB-2000 (first entry)

Db 1 ALYKKFKKKFLKS 13

RESULT 12
AY57468 standard; Peptide; 13 AA.

XX
ID AAY57468
AC AAY57468;
XX
DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-4 SEQ ID NO:6.

XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX
OS Synthetic.
OS Oryctolagus cuniculus.

XX
PN WO9942119-A1.

XX
PD 26-AUG-1999.

XX
PF 17-FEB-1999; 99WO-US03350.

XX
PR 18-FEB-1998; 98US-0025319.

XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX
PI Yeaman MR, Shen AJ;

XX
DR WO9942119-A1.

XX
PR 18-FEB-1998; 99WO-US03350.

XX
PT 17-FEB-1999; 99WO-US03350.

XX
PR 18-FEB-1998; 98US-0025319.

XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX
PI Yeaman MR, Shen AJ;

XX
PR WO9942119-A1.

XX
PS Disclosure; Page 108; 166pp; English.

XX
PS The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBBZBXB and its derivatives selected from XBBZBXBX, BXBXB, BXZBXB, XBBXBXBX and BBZBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXB, XBBXXBX, BXBBX, XBBZXB, and XBBZBXBXZBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AY57463 to AY57557 represent sequences used in the exemplification of the present invention.

XX
SQ Sequence 13 AA;

Query Match 69.6%; Score 48; DB 20; Length 13;
Best Local Similarity 69.2%; Pred. No. 0.77; 1; Mismatches 9; Conservative 3; Indels 0; Gaps 0;

OY 1 ALYKKWKNKLKS 13
Db 1 ARYRKFKNKLKS 13

RESULT 13
AY57467 standard; Peptide; 14 AA.

XX
AC AAY57467;
XX
DT 25-FEB-2000 (first entry)

Db 1 ALYKKFKKKFLKS 13

CC sequences used in the exemplification of the present invention.

XX

SQ sequence 18 AA;

Query Match 71.0%; Score 49; DB 20; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.75; 1; Mismatches 10; Conservative 1; Indels 2; Gaps 0;

OY 1 ALYKKWKNKLKS 13
Db 1 ALYKKFKKKLKLK 12

XX
DE Antimicrobial peptide RP-3 SEQ ID NO:5.
XX PD 26-AUG-1999.
KW PF 17-FEB-1999; 99WO-US03350.
XX PR 18-FEB-1998; 98US-0025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.
PS Disclosure; Page 108; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBKBXB and its derivatives selected from XBBZXBXB, BXZXB, BXZXZB, XBZXXB and BXZBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBZBXB, XBZXXBX, XBZXXB, and XBBZXXBXZBX; where B = at least one non polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.

CC Sequence 14 AA;

Query Match 59.6%; Score 48; DB 20; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.82;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY ||:|||||||
Db 2 LYKWKWNKLK 12

RESULT 14
AY57466 AAY57466 standard; Peptide: 13 AA..
ID DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-2 SEQ ID NO:4.
XX AC AAY57466;
XX AC AAY57466;
XX AC AAY57466;
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
PN WO9942119-A1.

XX Sequence 14 AA;

Query Match 69.6%; Score 48; DB 20; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.82;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY ||:|||||||
Db 2 LYRERFKNLK 12

RESULT 15
AY57503 AAY57503 standard; Peptide: 18 AA..
ID XX AC AAY57503;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
PN WO9942119-A1.

XX Sequence 13 AA;

Query Match 68.1%; Score 47; DB 20; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AYIKKKKLRS 13
DB 1 ARYKKFKKKLRS 13

RESULT 16
AY57503 AAY57503 standard; Peptide: 18 AA..
ID XX AC AAY57503;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
PN WO9942119-A1.

XX Sequence 13 AA;

Query Match 68.1%; Score 47; DB 20; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AYIKKKKLRS 13
DB 1 ARYKKFKKKLRS 13

RESULT 17
AY57503 AAY57503 standard; Peptide: 18 AA..
ID XX AC AAY57503;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
PN WO9942119-A1.

XX
DR
XX
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PT against bacteria and fungi

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XX Sequence 18 AA;

Query Match 68.1%; Score 47; DB 20; Length 18;
Best Local Similarity 76.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	ALYKKWKNLKLS	13
		:	
Db	1	ARYKFKKKLKS	13

Search completed: December 30, 2002, 16:22:09
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:21:13 ; Search time 16 Seconds
 (without alignments)
 78.109 Million cell updates/sec

Title: US-09-648-816B-9

Perfect score: 69

Sequence: 1 ALYKKWKNKLKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR:73;*

1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	49	71.0	445	2 C71636
2	44	63.8	827	2 F96647
3	43	62.3	445	2 G97846
4	42	60.9	245	2 A12126
5	42	60.9	397	2 S62579
6	42	60.9	579	2 B84956
7	41	59.4	286	2 D90609
8	41	59.4	531	2 T41151
9	40	58.0	87	2 AH1445
10	40	58.0	137	1 A36933
11	40	58.0	170	1 A33409
12	40	58.0	175	2 E82941
13	40	58.0	361	2 AC1437
14	40	58.0	453	2 H81151
15	40	58.0	453	2 D81870
16	39	56.5	119	2 D98013
17	39	56.5	162	1 A82911
18	39	56.5	277	2 H86589
19	39	56.5	277	2 C72033
20	39	56.5	338	2 T39635
21	39	56.5	342	2 T43038
22	39	56.5	439	2 T28196
23	39	56.5	487	4 S51886
24	39	56.5	492	2 S51885
25	39	56.5	528	4 S51887
26	39	56.5	569	2 S51685
27	39	56.5	569	2 E90554
28	39	56.5	560	2 S40098
29	39	56.5	759	2 T43031

ALIGNMENTS

RESULT 1

C71636 probable thiophene and furan oxidation protein thdf (thdF) RP759 - Rickettsia prowazekii

C;Species: Rickettsia prowazekii
 C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 02-Feb-2001
 C;Accession: C71636
 R;Andersson, S.G.E.; Zamorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
 Nature 356, 133-140, 1998
 A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A;Reference number: A71630; MUID:99039499; PMID:9823893
 A;Accession: C71636
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-445 <AND>
 A;Cross references: strain Madrid E
 A;Experimental source: strain Madrid E
 A;Genetics:
 A;Gene: thdF; RP759
 C;Superfamily: thiophene / furan oxidation protein; translation elongation factor Tu homology <ETU>
 C;Keywords: GTP binding; nucleotide-binding motif A (P-loop)
 F;216-332/Domain: translation elongation factor Tu homology <ETU>
 F;329-332/Region: GTP-binding NXXD motif
 F;329-332/Region: GTP-binding motif A (P-loop)

Query Match 71.0% Score 49; DB 2; Length 445;
 Best Local Similarity 72.7%; Pred. No. 2.1;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNKLK 12
 |||||:|||:
 Db 154 LYNNKWRNGLK 164

RESULT 2

F96647 hypothetical protein F19K23.5 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: F96647

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, A.; Hansen, N.F.; Hughes, B.; Hultzsch, L.; Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Maiti, R.; Marzella, R.; Mizro, M.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tali, A.; Wu, D.; Yu, G.; Fraser, C.M.; Ventner, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: F96647
 A;Status: preliminary

DNA topoisomerase

A; Molecule type: DNA
 A; Residues: 1-827 <SPO>
 A; Cross-references: GB:AE005173; NID:92160138; PIDN:AAE60760.1; GSPDB:GN00141
 C; Species: Schizosaccharomyces pombe
 A; Gene: F19K23.6
 A; Map position: 1

Query Match Similarity Score 63.8%; DB 2; Length 827;
 Best Local Similarity 61.5%; Pred. No. 26;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKNKLKS 13
 ||| :||| | | |
 Db 282 AMFKKWPNLTKS 294

RESULT 3

G97846 hypothetical protein thdf [imported] - Rickettsia conorii (strain Malish 7)
 C; Species: Rickettsia conorii
 C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
 C; Accession: G97846
 R; Ogata, H.; Audit, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001 Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A; Title: Reference number: A97700; MUID:21442074; PMID:11557893
 A; Accession: G97846
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-445 <KUR>
 A; Cross-references: GB:AE006914; PIDN:AAI03713.1; PID:915620303; GSPDB:GN00173
 C; Genetics:
 C; Gene: thdf
 C; Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu homolog
 Query Match Similarity Score 62.3%; DB 2; Length 445;
 Best Local Similarity 58.3%; Pred. No. 21;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKWKNKLKS 12
 ||| :||| | | |
 Db 153 ALNNNRSQLLK 164

RESULT 4

A12126 hypothetical protein all2568 [imported] - Nostoc sp. (strain PCC 7120)
 C; Species: Nostoc sp.
 A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C; Accession: A12126
 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurihara, T.; Sasamoto, S.; Watanabe, A.; Iriuchihara, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
 A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120
 A; Reference number: AB1807; MUID:21595285; PMID:11759840
 A; Accession: A12126
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-245 <KUR>
 A; Cross-references: GB:BA000019; PIDN:BA74267.1; PID:917131660; GSPDB:GN00179
 A; Experimental source: strain PCC 7120
 C; Genetics:
 C; Gene: all12568
 C; Superfamily: Synechocystis hypothetical protein srlr718
 Query Match Similarity Score 60.9%; DB 2; Length 245;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKWKNKLKS 11
 ||| :||| | |
 Db 189 ALYSOWONLL 199

RESULT 5

S62579 probable plasma membrane iron permease - fission yeast (Schizosaccharomyces pombe)
 C; Species: Schizosaccharomyces pombe
 C; Date: 16-May-1995 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000
 C; Accession: S62579; T38101
 R; Murphy, L.; Niblett, D.; Harris, D. submitted to the EMBL Data Library, November 1995
 A; Reference number: S62573
 A; Accession: S62579
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-397 <MUR>
 A; Cross-references: EMBL:Z67998; NID:91067202; PIDN:CAA91954.1; PID:91067209
 R; Beck, A.; Reinhardt, R.; Murphy, L.; Niblett, D.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Reference number: Z21769
 A; Accession: T38101
 A; Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: DNA
 A; Residues: 1-397 <MUR>
 A; Cross-references: EMBL:Z67998; NID:91067202; PIDN:CAA91954.1; GSPDB:GN00066; SPDB:S62579
 A; Experimental source: strain 92h-; cosmid c1F7
 C; Genetics:
 A; Gene: SPAC1C7.07C
 A; Map position: 1R
 C; Superfamily: conserved probable membrane protein YBR207w
 Query Match Similarity Score 60.9%; DB 2; Length 397;
 Best Local Similarity 58.3%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKS 13
 ||| :||| | | |
 Db 118 LQEKRKKLMKS 129

RESULT 6

B84956 cell division protein fts1 [imported] - Buchnera sp. (strain APS)
 C; Species: Buchnera sp.
 C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C; Accession: B84956
 R; Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakai, Y.; Ishikawa, H.; Nature 407, 81-86, 2000
 A; Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
 A; Reference number: A84930; MUID:20445173; PMID:1093077
 A; Accession: B84956
 A; Status: Preliminary
 A; Molecule type: DNA
 A; Residues: 1-579 <SPO>
 A; Cross-references: GB:AP000398; GSPDB:GN00144
 A; Experimental source: strain APS
 C; Genetics:
 A; Gene: fts1; BU222
 C; Superfamily: penicillin-binding protein 3
 Query Match Similarity Score 60.9%; DB 2; Length 579;
 Best Local Similarity 66.7%; Pred. No. 39;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKS 13
 ||| :||| | | |
 Db 1 MYKKERNFRKKS 12

RESULT 7

D06069 conserved hypothetical protein MYPU_7800 [imported] - Mycoplasma pulmonis (strain UAB)
 C; Species: Mycoplasma pulmonis
 C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;	C;Accession: D90609	C;Genetics: A;Gene: lin0103
Nucleic Acids Res. 29, 2145-2153, 2001	C;Species: Schizosaccharomyces pombe	C;Species: Streptococcus mutans
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm	C;Accession: A99512; MUID:21267165; PMID:11353084	C;Accession: A36933; MUID:94012483; PMID:8407794
A;Status: preliminary	A;Residues: 1-286 <KUR>	A;Status: preliminary
A;Molecule type: DNA	A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153	A;Molecule type: DNA
A;Experimental source: strain UAB CTP	C;Accession: A99512; MUID:21267165; PMID:11353084	C;Accession: A99512; MUID:21267165; PMID:11353084
C;Genetics:	C;Genetics:	C;Genetics:
A;Gene: MYPU_7800	A;Gene: SGc3	A;Gene: SGc3
RESULT 8	Query Match 59.4%; Score 41; DB 2; Length 286;	Query Match 58.0%; Score 40; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 28; Length 286;	Best Local Similarity 85.7%; Pred. No. 13; Length 87;	A;Gene: A36933
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	C;Species: Streptococcus mutans
OY 2 LYKKWKWLK 12 ::I :	OY 3 YKKWKNK 9	C;Accession: A36933
Db 137 IWKWKNQNLK 147	Db 77 YKKWNENK 83	R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.
T41151	Lysyl-tRNA synthetase - fission yeast (Schizosaccharomyces pombe)	J. Bacteriol. 175, 6220-6228, 1993
C;Species: Schizosaccharomyces pombe	C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000	A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir
C;Accession: T41151	R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.	A;Reference number: A36933; MUID:94012483; PMID:8407794
R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.	submitted to the EMBL Data Library, October 1998	A;Contents: GS5
A;Status: preliminary	A;Status: preliminary	A;Accession: A36933
A;Molecule type: DNA	A;Molecule type: DNA	A;Status: preliminary
A;Residues: 1-531 <HLI>	A;Residues: 1-137 <YAM>	A;Molecule type: DNA
A;Cross-references: EMBL:AL031907; PIDN:CAA21422.1; GSPDB:GN00068; SPDB:SPCC18.08	A;Note: sequence extracted from NCBI backbone (NCBIN:138054, NCBI:P:138056)	A;Residues: 1-137 <YAM>
A;Experimental source: strain 972h; cosmid C18	C;Superfamily: Bacillus subtilis diacylglycerol kinase dgKA	A;Note: sequence extracted from NCBI backbone (NCBIN:138054, NCBI:P:138056)
C;Genetics:	Query Match 58.0%; Score 40; DB 1; Length 137;	C;Superfamily: Bacillus subtilis diacylglycerol kinase dgKA
A;Gene: SPDB:SPCC18.08	Best Local Similarity 70.0%; Pred. No. 20; Length 137;	A;Accession: A36933; MUID:94012483; PMID:8407794
C;Map position: 3	Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	A;Accession: A36933
C;Superfamily: lysine-tRNA ligase	OY 4 KWKWNKLKS 13 ::I :	A;Status: preliminary
Query Match 59.4%; Score 41; DB 2; Length 531;	Db 13 KWKWNKLTS 22	A;Molecule type: DNA
Best Local Similarity 50.0%; Pred. No. 53; Length 531;	OY 5 KWKWNKLTS 22	A;Residues: 1-137 <YAM>
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	Db 13 KWKWNKLTS 22	A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153
OY 2 LYKKWNKLKS 13 ::I :	OY 5 KWKWNKLTS 22	A;Experimental source: strain C18
Db 66 IIEKWRNKTKS 77	Db 13 KWKWNKLTS 22	C;Accession: A99512; MUID:21267165; PMID:11353084
RESULT 9	Query Match 58.0%; Score 40; DB 2; Length 170;	C;Species: Listeria innocua
AH1445 hypothetical protein lln0103 [imported] - Listeria innocua (strain C18pl1262)	Best Local Similarity 63.6%; Pred. No. 24; Length 170;	C;Accession: A36933; MUID:94012483; PMID:8407794
C;Species: Listeria innocua	Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	A;Gene: BMEI1257
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001	A;Map position: I	A;Genetics:
C;Accession: AH1445	Query Match 58.0%; Score 40; DB 2; Length 170;	A;Accession: BMEI1257
R;Glaser, P.; Franpeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001	Best Local Similarity 63.6%; Pred. No. 24; Length 170;	A;Map position: I
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourna, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of Listeria species	Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	A;Map position: I
A;Reference number: AB1077; MUID:2153729; PMID:11679669	OY 1 ALYKKWNKL 11 ::I :	A;Accession: BMEI1257
A;Status: preliminary	Db 9 AVYNNOKNL 19	A;Molecule type: DNA
A;Molecule type: DNA	OY 1 ALYKKWNKL 11 ::I :	A;Residues: 1-170 <KUR>
A;Residues: 1-87 <GLA>	Db 9 AVYNNOKNL 19	A;Cross-references: GB:AL008917; PIDN:AA152438.1; PID:917983242; GSPDB:GN00190
A;Cross-references: GB:AL592022; PIDN:CAC95336.1; PID:916412523; GSPDB:GN00178	A;Experimental source: strain C18pl1262	A;Experimental source: strain C18
A;Experimental source: strain C18pl1262	C;Accession: A99512; MUID:21267165; PMID:11353084	C;Accession: A99512; MUID:21267165; PMID:11353084
RESULT 10	Query Match 58.0%; Score 40; DB 2; Length 87;	C;Species: Ureaplasma urealyticum
A36933	Best Local Similarity 85.7%; Pred. No. 13; Length 87;	C;Species: Ureaplasma urealyticum
dicylglycerol kinase homolog - Streptococcus mutans	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	C;Accession: A36933
C;Species: Streptococcus mutans	A;Gene: A36933	R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.
C;Accession: A36933	C;Accession: A36933	J. Bacteriol. 175, 6220-6228, 1993
R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.	A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir	A;Reference number: A36933; MUID:94012483; PMID:8407794
J. Bacteriol. 175, 6220-6228, 1993	A;Contents: GS5	A;Accession: A36933
A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir	A;Accession: A36933	A;Status: preliminary
A;Reference number: A36933; MUID:94012483; PMID:8407794	A;Status: preliminary	A;Molecule type: DNA
A;Contents: GS5	A;Accession: A36933	A;Residues: 1-137 <YAM>
A;Accession: A36933	A;Accession: A36933	A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153
A;Status: preliminary	A;Status: preliminary	A;Experimental source: strain C18
A;Map position: I	A;Map position: I	C;Accession: A99512; MUID:21267165; PMID:11353084
RESULT 11	Query Match 58.0%; Score 40; DB 2; Length 137;	C;Species: Brucella melitensis
A36939	Best Local Similarity 70.0%; Pred. No. 20; Length 137;	C;Accession: A36939
dinB protein [imported] - Brucella melitensis (strain 16M)	Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	C;Accession: A36939
C;Species: Brucella melitensis	OY 4 KWKWNKLKS 13 ::I :	R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
C;Accession: A36939	Db 13 KWKWNKLTS 22	; Mazur, M.; Goitsman, E.; Selkov, E.; Elzer, P.H.; Hagiwara, S.; O'Callaghan, D.; Let
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov	Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002	Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
; Mazur, M.; Goitsman, E.; Selkov, E.; Elzer, P.H.; Hagiwara, S.; O'Callaghan, D.; Let	A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit	A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002	A;Reference number: A03252; PMID:11756688	A;Reference number: A03252; PMID:11756688
A;Accession: A36939	A;Accession: A36939	A;Status: preliminary
A;Status: preliminary	A;Status: preliminary	A;Molecule type: DNA
A;Molecule type: DNA	A;Accession: A36939	A;Residues: 1-170 <KUR>
A;Residues: 1-170 <KUR>	A;Accession: A36939	A;Cross-references: GB:AE008917; PIDN:AA152438.1; PID:917983242; GSPDB:GN00190
A;Cross-references: GB:AE008917; PIDN:AA152438.1; PID:917983242; GSPDB:GN00190	A;Experimental source: strain C18	A;Experimental source: strain C18
A;Experimental source: strain C18	C;Accession: A36939	C;Accession: A36939
C;Accession: A36939	A;Gene: BMEI1257	A;Gene: BMEI1257
A;Gene: BMEI1257	A;Map position: I	A;Map position: I
A;Map position: I	Query Match 58.0%; Score 40; DB 2; Length 170;	A;Accession: A36939
RESULT 12	Best Local Similarity 63.6%; Pred. No. 24; Length 170;	C;Species: Ureaplasma urealyticum
E82941 hypothetical protein DU032 [imported] - Ureaplasma urealyticum	Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum	OY 1 ALYKKWNKL 11 ::I :	C;Accession: A36939
C;Accession: A36939	Db 9 AVYNNOKNL 19	R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.
R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.	OY 1 ALYKKWNKL 11 ::I :	J. Bacteriol. 175, 6220-6228, 1993
J. Bacteriol. 175, 6220-6228, 1993	Db 9 AVYNNOKNL 19	A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir
A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir	OY 1 ALYKKWNKL 11 ::I :	A;Contents: GS5
A;Contents: GS5	Db 9 AVYNNOKNL 19	A;Accession: A36939
A;Accession: A36939	OY 1 ALYKKWNKL 11 ::I :	A;Status: preliminary
A;Status: preliminary	Db 9 AVYNNOKNL 19	A;Molecule type: DNA
A;Molecule type: DNA	OY 1 ALYKKWNKL 11 ::I :	A;Residues: 1-137 <YAM>
A;Residues: 1-87 <GLA>	Db 9 AVYNNOKNL 19	A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153
A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153	A;Experimental source: strain C18	A;Experimental source: strain C18
A;Experimental source: strain C18	C;Accession: A36939	C;Accession: A36939
C;Accession: A36939	A;Gene: BMEI1257	A;Gene: BMEI1257
A;Gene: BMEI1257	A;Map position: I	A;Map position: I
A;Map position: I	Query Match 58.0%; Score 40; DB 2; Length 170;	A;Accession: A36939
RESULT 13	Best Local Similarity 63.6%; Pred. No. 24; Length 170;	C;Species: Ureaplasma urealyticum
E82942 hypothetical protein DU032 [imported] - Ureaplasma urealyticum	Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum	OY 1 ALYKKWNKL 11 ::I :	C;Accession: A36939
C;Accession: A36939	Db 9 AVYNNOKNL 19	R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.
R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.	OY 1 ALYKKWNKL 11 ::I :	J. Bacteriol. 175, 6220-6228, 1993
J. Bacteriol. 175, 6220-6228, 1993	Db 9 AVYNNOKNL 19	A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir
A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir	OY 1 ALYKKWNKL 11 ::I :	A;Contents: GS5
A;Contents: GS5	Db 9 AVYNNOKNL 19	A;Accession: A36939
A;Accession: A36939	OY 1 ALYKKWNKL 11 ::I :	A;Status: preliminary
A;Status: preliminary	Db 9 AVYNNOKNL 19	A;Molecule type: DNA
A;Molecule type: DNA	OY 1 ALYKKWNKL 11 ::I :	A;Residues: 1-137 <YAM>
A;Residues: 1-87 <GLA>	Db 9 AVYNNOKNL 19	A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153
A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153	A;Experimental source: strain C18	A;Experimental source: strain C18
A;Experimental source: strain C18	C;Accession: A36939	C;Accession: A36939
C;Accession: A36939	A;Gene: BMEI1257	A;Gene: BMEI1257
A;Gene: BMEI1257	A;Map position: I	A;Map position: I
A;Map position: I	Query Match 58.0%; Score 40; DB 2; Length 170;	A;Accession: A36939
RESULT 14	Best Local Similarity 63.6%; Pred. No. 24; Length 170;	C;Species: Ureaplasma urealyticum
E82943 hypothetical protein DU032 [imported] - Ureaplasma urealyticum	Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum	OY 1 ALYKKWNKL 11 ::I :	C;Accession: A36939
C;Accession: A36939	Db 9 AVYNNOKNL 19	R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.
R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.	OY 1 ALYKKWNKL 11 ::I :	J. Bacteriol. 175, 6220-6228, 1993
J. Bacteriol. 175, 6220-6228, 1993	Db 9 AVYNNOKNL 19	A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir
A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir	OY 1 ALYKKWNKL 11 ::I :	A;Contents: GS5
A;Contents: GS5	Db 9 AVYNNOKNL 19	A;Accession: A36939
A;Accession: A36939	OY 1 ALYKKWNKL 11 ::I :	A;Status: preliminary
A;Status: preliminary	Db 9 AVYNNOKNL 19	A;Molecule type: DNA
A;Molecule type: DNA	OY 1 ALYKKWNKL 11 ::I :	A;Residues: 1-137 <YAM>
A;Residues: 1-87 <GLA>	Db 9 AVYNNOKNL 19	A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153
A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153	A;Experimental source: strain C18	A;Experimental source: strain C18
A;Experimental source: strain C18	C;Accession: A36939	C;Accession: A36939
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A;Gene: BMEI1257	A;Map position: I	A;Map position: I
A;Map position: I	Query Match 58.0%; Score 40; DB 2; Length 170;	A;Accession: A36939
RESULT 15	Best Local Similarity 63.6%; Pred. No. 24; Length 170;	C;Species: Ureaplasma urealyticum
E82944 hypothetical protein DU032 [imported] - Ureaplasma urealyticum	Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum	OY 1 ALYKKWNKL 11 ::I :	C;Accession: A36939
C;Accession: A36939	Db 9 AVYNNOKNL 19	R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.
R;Yamashita, I.; Takehara, T.; Kuramitsu, H.K.	OY 1 ALYKKWNKL 11 ::I :	J. Bacteriol. 175, 6220-6228, 1993
J. Bacteriol. 175, 6220-6228, 1993	Db 9 AVYNNOKNL 19	A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir
A;Title: Molecular characterization of a Streptococcus mutans mutant altered in envir	OY 1 ALYKKWNKL 11 ::I :	A;Contents: GS5
A;Contents: GS5	Db 9 AVYNNOKNL 19	A;Accession: A36939
A;Accession: A36939	OY 1 ALYKKWNKL 11 ::I :	A;Status: preliminary
A;Status: preliminary	Db 9 AVYNNOKNL 19	A;Molecule type: DNA
A;Molecule type: DNA	OY 1 ALYKKWNKL 11 ::I :	A;Residues: 1-137 <YAM>
A;Residues: 1-87 <GLA>	Db 9 AVYNNOKNL 19	A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153
A;Cross-references: GB:AL445566; PID:914090195; PIDN:CAC13953.1; GSPDB:GN00153	A;Experimental source: strain C18	A;Experimental source: strain C18
A;Experimental source: strain C18	C;Accession: A36939	C;Accession: A36939
C;Accession: A36939	A;Gene: BMEI1257	A;Gene: BMEI1257
A;Gene: BMEI1257	A;Map position: I	A;Map position: I
A;Map position: I	Query Match 58.0%; Score 40; DB 2; Length 170;	A;Accession: A36939

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: ED2941
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
 A;Reference number: A82870
 A;Accession: ED2941
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-175 <GLA>
 A;Cross-references: GB:AE002103; GR:AF222894; NID:96898977; PIDN:AAF30437.1; GSPDB:GN001
 A;Experimental source: serovar 3; biovar 1
 C;Genetics:
 A;Gene: UU032
 A;Genetic code: SGC3

Query Match 58.0%; Score 40; DB 2; Length 175;
 Best Local Similarity 75.0%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LYKKWNKNK 9
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 Db 70 VVKKWNKNK 77

RESULT 13

AC1437
 C;Species: Glucosamine-fructose-6-phosphate aminotransferase (C-terminal domain) homolog lin0034 [i]
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
 C;Accession: AC1437
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kretf, J.; Kuhn, M.; Kunst, F.; Kurakpat, G.; Madueno, E.; Maitouram, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierre, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:2153729; PMID:11679659
 A;Accession: AC1437
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-361 <GLA>
 A;Cross-references: GB:AL592022; PTN:CAC95267.1; PID:916412455; GSPDB:GN00178
 A;Experimental source: strain clipp11262
 C;Genetics:
 A;Gene: lin0034

Query Match 58.0%; Score 40; DB 2; Length 361;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKKWNKNK 9
 :||| |||||:
 Db 200 AFYERWKWNE 208

RESULT 14

H81151
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C;Accession: H81151
 R;Bettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hori, H.; Qin, H.; Yamatievean, J.; Gill, J.; Scariato, V.; Masison, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; ve
 A;Title: Complete genome sequence of *Neisseria meningitidis* Serogroup B strain MC58.
 A;Reference number: AB1000; MUID:20175755; PMID:10710307
 A;Accession: H81151
 A;Status: preliminary
 A;Molecule type: DNA

Query Match 58.0%; Score 40; DB 2; Length 453;
 Best Local Similarity 58.3%; Pred. No. 65;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 LYKKWNKNLKS 13
 :||| |||:|||:
 Db 1 MLKKWLNLKMLPS 12

A;Residues: 1-453 <TER>
 A;Cross-references: GB:AE002437; GB:AE002098; NID:97226072; PIDN:AAF41254.1; PID:g7722
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB843

Query Match 58.0%; Score 40; DB 2; Length 453;
 Best Local Similarity 58.3%; Pred. No. 65;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 LYKKWNKNLKS 13
 :||| |||:|||:
 Db 1 MLKKWLNLKMLPS 12

Search completed: December 30, 2002, 16:23:26
 Job time : 18 secs

GenCore version 5.1.3 Copyright (C) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2002, 16:18:28 ; Search time 11 Seconds (without alignments)

Post-processing: Minimum Match 0%

Maximum DB seq length: 2000000000

Database : Swissprot_40; *

Perfect score: US-09-648-816B-9

Sequence: 1 ALYKKWNKLKKS 13

Scoring table: BLOSSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query Length	DB ID	Description
1	49	71.0	445	TRME_RICPR
2	43	62.3	445	TRME_RICCN
3	42	60.9	245	COMB_ANASCH
4	42	60.9	397	YAKI_SCCHPO
5	42	60.9	1	FTSI_BUCA1
6	42	60.9	1971	MCA1_MOUSE
7	40	58.0	1371	RDGL_STRMU
8	40	58.0	175	Y032_UREPA
9	39	56.5	293	VBL1_BGMV
10	39	56.5	569	SYE_TOBAC
11	39	75.9	1	TOP3_CAEEL
12	39	56.5	1215	BGCN_DRONE
13	39	56.5	1253	SC25_YEAST
14	38	55.1	180	Y426_METJA
15	38	55.1	185	Y754_METJA
16	38	55.1	252	ORC6_HUMAN
17	38	55.1	262	ORC6_MOUSE
18	38	55.1	293	VBL1_SLCV
19	38	55.1	969	DPOM_NEUTN
20	38	55.1	2514	POLN_SINDO
21	37	53.6	90	PLF4_PINGO
22	37	53.6	130	YGB5_YEAST
23	37	53.6	249	MCT1_CANFA
24	37	53.6	264	SCHPO
25	37	53.6	347	YJ91_YEAST
26	37	53.6	377	Y412_MIGCE
27	37	53.6	473	MVIN_THEMEA
28	37	53.6	645	REP_BUCA1
29	37	53.6	785	PTAI1_YEAST
30	37	53.6	792	SYL1_WYCCE
31	37	53.6	878	IL13B_MOUSE
32	37	53.6	896	CYR6_MOUSE
33	37	53.6	1068	YCF0_MARPO

SUMMARIES

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	445 AA.
TRME_RICPR				
ID	Q9ZC11;			
AC				
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Probable tRNA modification GTPase TRME.			
DE	TRME OR THDF OR RP759.			
GN				
OS	Rickettsia prowazekii			
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;			
OC	Rickettsiaceae; Rickettsiae; Rickettsia.			
OX				
RN	Ncbi_TaxID=82;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RA	STRAIN=Madrid E;			
RA	MEOLINE-99039499; PubMed=9923893;			
RA	Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of mitochondria"; Nature 396:133-140(1998).			
RT				
RL				
CC	-!- FUNCTION: EXHIBITS A VERY HIGH INTRINSIC GTPASE HYDROLYSIS RATE.			
CC	INVOLVED IN THE BIOSYNTHESIS OF THE HYPERMODIFIED NUCLEOSIDE 5'-METHYLAMINOMETHYL-2'-THIORIDINE, WHICH IS FOUND IN THE WOBBLE POSITION OF SOME tRNAs (BY SIMILARITY).			
CC	-!- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING PROTEINS. TRME SUBFAMILY.			
CC				
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CC				
CC	EMBL; AJ235273; CAA15187; 1; -			
CC	DR; InterPro; IPR00589; GTP-binding_domain.			
CC	DR; InterPro; IPR00591; MNR_HSL1.			
CC	DR; InterPro; IPR00525; Small_GTP.			
CC	DR; InterPro; IPR004520; ThdF.			
CC	Pfam; PF01936; MNR_HSL1; 1.			
DR	DR; TIGRFAMS; TIGR00231; Small_GTP; 1.			
DR	TIGRFAMS; TIGR00450; ThdF; 1.			
DR	TIGRFAMS; TIGR00450; MG442; 1.			
KW	tRNA processing; GTP-binding; complete proteome.			
FT	NP_BIND	222	229	GTP (POTENTIAL).
FT	NP_BIND	269	273	GTP (POTENTIAL).
FT	NP_BIND	329	332	GTP (POTENTIAL).
FT	SEQUENCE	445 AA:	49813 MW:	FA15B99E716B4F6 CRC64;
Best Local Similarity	72.7%	Score 49;	DB 1;	Length 445;
Matches	8;	Conservative	2;	Mismatches 1; Indels 0; Gaps 0;

RA Skelton J., Simmonds M., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voelker G., Aert R., Robins J., Grimonprez B.,
 RA Weltjens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Egger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Coffeau A., Cadieu E., Dreano S., Gloux S., Delaune V., Mottier S.,
 RA Galibert F., Avies S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Cerruti L., Lowe T., McCombe W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of *Schizosaccharomyces pombe*";
 RL Nature 415:871-880(2002);
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE FTR1 FAMILY.
 CC
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 CC
 DR EMBL; AP00118; BAB12938.1;
 DR InterPro; IPR00311; PBP_dimer.
 DR InterPro; IPR001460; transpeptidase.
 DR Pfam; PF00905; transpeptidase; 1.
 DR Pfam; PF03717; PBP_dimer; 1.
 KW Transmembrane; Peptidoglycan synthesis; Cell division; Cell wall;
 KW Multifunctional enzyme; Cell shape; Complete proteome;
 FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 22 42 POTENTIAL.
 FT DOMAIN 43 579 EXTRACELLULAR (POTENTIAL).
 FT ACT SITE 305 305 ACTIVATED BY PENICILLIN (BY SIMILARITY).
 SQ SEQUENCE 579 AA: 65204 MW: E3717820808CAD12 CRC64;
 Query Match 60.9%; Score 42; DB 1; Length 579;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 LYKKWKNKLKS 13
 Db 1 MYKKEKNFLKS 12
 RESULT 5
 FTSI_BUCA1 STANDARD:
 AC FTSI_BUCA1 PRT: 579 AA.
 ID FTSI_BUCA1 PRT: 579 AA.
 AC P5317;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidoglycan synthetase ftsi (Penicillin-binding protein 3) (PBP-3).
 GN FTSI OR BU222.
 OS Buchnera aphidicola (subsp. *Acyrthosiphon pisum*) (*Acyrthosiphon pisum* symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OC NCBI_TaxID=118099;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=TOKYO 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakai Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. A.P.S.";
 RL Nature 407:81-85(2000).
 CC -!- FUNCTION: CELL WALL FORMATION, ESSENTIAL FOR THE FORMATION OF A
 CC -!- SEPTUM OF THE MUREIN SACCULUS. SYNTHESIS OF CROSS-LINKED
 CC PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES (BY SIMILARITY).
 CC -!- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated (Potential)
 CC -!- DOMAIN: HAS AN N-TERMINAL PENICILLIN INSENSITIVE TRANSGLYCOSYLASE
 CC

RA DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) & A CARBOXY-TERMINAL
 RA PEPTICULIN-SENSITIVE TRANSEPTIDASE DOMAIN (CROSS-LINKING OF THE
 RA PEPTIDE SUBUNITS).
 RA -!- SIMILARITY: BELONGS TO THE TRANSEPTIDASE FAMILY.
 RA
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 RA or send an email to license@isb-sib.ch).
 RA
 DR EMBL; AP00118; BAB12938.1;
 DR InterPro; IPR00311; PBP_dimer.
 DR InterPro; IPR001460; transpeptidase.
 DR Pfam; PF00905; transpeptidase; 1.
 DR Pfam; PF03717; PBP_dimer; 1.
 KW Transmembrane; Peptidoglycan synthesis; Cell division; Cell wall;
 KW Multifunctional enzyme; Cell shape; Complete proteome;
 FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 22 42 POTENTIAL.
 FT DOMAIN 43 579 EXTRACELLULAR (POTENTIAL).
 FT ACT SITE 305 305 ACTIVATED BY PENICILLIN (BY SIMILARITY).
 SQ SEQUENCE 579 AA: 65204 MW: E3717820808CAD12 CRC64;
 Query Match 60.9%; Score 42; DB 1; Length 579;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 LYKKWKNKLKS 13
 Db 1 MYKKEKNFLKS 12
 RESULT 6
 MC3A_MOUSE STANDARD:
 ID MC3A_MOUSE PRT: 1971 AA.
 AC Q9WUQ9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 80 kDa MCM3-associated protein (GANP protein).
 GN MCM3AP OR GANP OR MAP80.
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=BALB/C X NZB;
 RX MEDLINE=20197882; PubMed=10733502;
 RA Kuwahara K., Yoshida M., Kondo E., Sakata A., Watanabe Y., Abe E.,
 RA Kouno Y., Tomiyasu S., Fujimura S., Tokunisa T., Kimura H., Ezaki T.,
 RA Sakaguchi N.;
 RT "A novel nuclear phosphoprotein, GANP, is up regulated in centrocytes
 RT of the germinal center and associated with MCM3, a protein essential
 RT for DNA replication.";
 RL Blood 95:2321-2328(2000).
 CC -!- FUNCTION: MAY BE INVOLVED IN THE NUCLEAR LOCALIZATION PATHWAY OF
 CC MCM3 (BY SIMILARITY).
 CC -!- SUBUNIT: INTERACTS WITH MCM3.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -!- PTM: PHOSPHORYLATED (PROBABLE).
 CC -!- SIMILARITY: BELONGS TO THE SAC3 FAMILY.
 CC
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CC	DR	EMBL; AE006590; CAB44241.1; -.
CC	MGD	MGI:1930089; Mcm3bp.
CC	InterPro	IPR005062; SAC3_GANP.
CC	DR	Pfam: PF03399; SAC3_GANP; 1.
KW	Nuclear protein, Phosphorylation.	SEQUENCE 1971 AA; 217138 MW; 5F342E256C007E24 CRC64;
SQ	Query Match 60.9%; Score 42; DB 1; Length 1971; Best Local Similarity 77.8%; Pred. No. 53; 1; Mismatches 7; Conservative 1; Indels 0; Gaps 0;	78 POTENTIAL. CYTOPLASMIC (POTENTIAL).
QY	3 YKKWNKLL 11	108 POTENTIAL.
Db	1710 YQKWNKSL 1718	129 LL-> VP (IN REF. 2).
RESULT 7		128 15380 MW; 4F01654885319125 CRC64;
KDGL_STRMU	STANDARD; PRT; 137 AA.	137 AA; 15380 MW; 4F01654885319125 CRC64;
ID		13 KRWKNRLTS 22
KGDL_STRMU		
AC	00588; 051807; (Rel. 28, Created)	
DT	01-FEB-1994 (Rel. 28, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)	
DE	Diacetylglycerol kinase (EC 2.7.1.107) (DAGK) (Diacylglyceride kinase)	
DE	(DGK).	
GN	DGKA or DGK.	
GN	Streptococcus mutans.	
OC	Bacterium; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
OX	NCBI_TaxID=1309;	
RN	[1] SEQUENCE FROM N.A.	
RP	STRAIN=GS-5; PubMed=8407794;	
RX	MEDLINE=94012483; Pubmed=8407794;	
RA	Yamashita Y., Takehara T., Kuramitsu H.K.;	
RA	"Molecular characterization of a Streptococcus mutans mutant altered	
RT	in environmental stress responses";	
RT	J. Bacteriol. 175:6220-6228(1993).	
RN	[2] SEQUENCE FROM N.A.	
RP	STRAIN=T8;	
RC	SEQUENCE FROM N.A.	
RX	MEDLINE=94083071; PubMed=9422608;	
RA	Chen P., Novak J.J., Oi F.-O., Caufield P.W.;	
RT	"Diacylglycerol kinase is involved in regulation of expression of the	
RT	lantibiotic mutacin II of Streptococcus mutans";	
RL	J. Bacteriol. 180:167-170(1998).	
CC	-!- FUNCTION: diacylglycerol produced during the	
CC	turnover of membrane phospholipid. May play a role in adaptability	
CC	to environmental stress conditions such as acid tolerance,	
CC	elevated temperatures and high osmolarity.	
CC	-!- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-	
CC	diacylglycerol 3-phosphate.	
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)	
CC	-!- SIMILARITY: BELONGS TO THE BACTERIAL DIACYLGLYCEROL KINASE FAMILY.	
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-!- EMBL; AE002103; AAF30437.1; -.	
DR	Hypothetical protein; Complete proteome.	
SQ	SEQUENCE 175 AA; 20950 MW; 93FDAD28712E5222 CRC64;	
QY	2 LYKKWKNK 9	
Db	70 VYKWNK 77	
RESULT 9		
VBL1_BGMV	STANDARD; PRT; 293 AA.	
ID	VBL1_BGMV	
AC	P0001;	
DT	13-AUG-1987 (Rel. 05, Created)	
DT	13-AUG-1987 (Rel. 05, Last sequence update)	
DT	01-JUN-1994 (Rel. 29, Last annotation update)	
DE	B1.1 protein (33.1 kDa Protein).	
GN	B1.1.	
OS	Bean golden mosaic virus.	
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.	
OX	NCBI_TaxID=10839;	
RN	[1] SEQUENCE FROM N.A.	
RP		

RA Howarth A.J.; Carton J.; Bosser M.; Goodman R.M.;
 RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
 regulation in geminiviruses.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
 CC !- SIMILARITY: BELONGS TO GEMINIVIRUSES BLI PROTEIN FAMILY.
 CC
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 CC
 CC
 DR EMBL; M10080: AAA46323.1; -.
 DR InterPro; IPR000211; Gemini_BLI.
 DR Pfam; PF00845; Gemini_BLI_1.
 SO SEQUENCE 293 AA; 33099 MW; CC3C4E0E93A79441 CRC64;
 Query Match 56.5%; Score 39; DB 1; Length 569;
 Best Local Similarity 61.5%; Pred. No. 50; Matches 8; Conservatve 3; Mismatches 2; Indels 0; Gaps 0;
 DR Db 141 ALYKQFAEKLLQS 153
 Oy 3 YKKWKNKLKS 13
 | ||| |||||
 Db 178 YGKWERKLIRS 188
 RESULT 10
 SYE_TOBAC STANDARD; PRT; 569 AA.
 TD SIE_TOBAC
 AC 043794;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
 DE (GluRS).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. SRL; TISSUE=Leaf;
 RA Andersen R.V.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC !- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamyl-tRNA(Glu).
 CC !- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC
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 CC
 DR EMBL; X83524; CAA88506.1; -.
 DR HSSP; P27000; 1GLN
 DR InterPro; IPR00527; GLTX_bact.
 DR InterPro; IPR000924; Glu_tRNA-synt_1c.
 DR InterPro; IPR01412; tRNA-synt_1c.
 DR Pfam; PF00749; tRNA-synt_1c_1.
 DR PRINTS; PR0087; TRNASCNTHGJU.
 DR TIGRFAMS; TIGR00464; gltx_bact; 1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 DR Amidoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SITE 62 "HIGH" REGION.
 FT SITE 303 307 "KSKSKS" REGION.
 FT BINDING 306 306 ATP (BY SIMILARITY).
 SO SEQUENCE 569 AA; 63338 MW; F2E81D73460A1844 CRC64;
 Query Match 56.5%; Score 39; DB 1; Length 759;
 Best Local Similarity 60.0%; Pred. No. 66; Matches 6; Conservatve 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKKNKL 11
 :||| :|||
 AC 09W112; 09W113;
 DB 455 VWEKWNRL 464

RESULT 12
 BGNCN_DROME STANDARD; PRT; 1215 AA.

ID BGNCN_DROME
 AC 09W112; 09W113;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Benign gonial cell neoplasm protein.
 GN BGNCN OR B2)GCN OR C030170/CG0331.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscoidea; Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TAXID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-testis;
 RX MEDLINE=20304590; PubMed=10924476;
 RA Ollstein B., Lavoie C.A., Vef O., Gaterf E., McKeearin D.M.;
 RT "the Drosophila cystoblast differentiation factor, benign gonial cell
 neoplasm, is related to DEXH-box proteins and interacts genetically
 with bag-of-marbles.";
 RL Genetics 155:1809-1815 (2000).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinkiner S.E., Holt R.A., Evans C.A., cocayne J.D.,
 Ananatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Suttorp G.G., Wortsman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazier R.G., Champe M., Preiffer B.D.,
 RA Wan K.H., Doyle C., Baxter G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Akgavani A., An H.-J., Andevs-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhakrati D., Bolhakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
 RA Burts C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Danile C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew T., Dietz S.M.,
 RA Dousou K., Douc L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabreidian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskeen D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simonds M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska S., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M.,梵特 J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]

RP REVISIONS.

RC STRAIN-Berkeley;
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celinkiner S.E.,
 RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
 RA Harris N.L., Kromoller B., Marshall B., Millburn G.H., Richter J.,
 RA Russo S., Kromoller B., Marshall B., Shiu S., Smutniak F., Rubin G.M.,
 RA Mungall C.J., Lewis S.E.;
 RT Annotation of Drosophila melanogaster genome."
 RL Submitted (MAY-2002) to the EMBL/Genbank/DDBJ databases.
 CC -!- FUNCTION: ESSENTIAL CYSTOBLAST DIFFERENTIATION FACTOR REQUIRED FOR
 CC BAM FUNCTION IN ASYMMETRIC DIVISION OF THE GERMLINE STEM CELLS.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND IN 5-8 GERMLINE STEM
 CC CELLS OF OVARIES IMMEDIATELY ADJACENT TO TERMINAL FILAMENT.
 CC -!- SIMILARITY: SOME SIMILARITIES TO DEXH-BOX PROTEINS BUT OUTSIDE OF
 CC THE HELICASE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 ANK REPEAT.
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 CC -----
 DR EMBL; AF255662; AFAF9148.1; .
 DR EMBL; AE03463; AFAF4707.2; .
 DR Flybase; FBgn0004581; bgcn.
 DR InterPro; IPR002110; ANK.
 DR pfam; PF00023; ank; 2.
 DR SMART; SM00248; ANK; 1.
 DR PROSITE; PS50297; ANK REP-REGION; 1.
 DR PS50088; ANK REPET; 1.
 RW Developmental protein; ANK repeat.
 SQ FT REPEAT 407 439 ANK.
 REPEAT 407 439 ANK.
 SEQUENCE 1215 AA; 139278 MW; 11F83C1B3816F2CD CRC64;
 Query Match 56.5%; Score 3.9; DB 1; Length 1215;
 Best Local Similarity 55.6%; Pred. No. 1e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 2 LYKKKNKL 10
 | ||:||:
 DB 792 LYKEWONR 800

RESULT 13
 SC25_YEAST STANDARD; PRT; 1253 AA.

ID SC25_YEAST
 AC PI4771;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1995 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE SCD25 protein.
 GN SCD25 OR SPC25 OR YIL016W
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Saccharomyces; Fundi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC SCD25_YEAST; SCD25; SCD25_YEAST
 RN OBL1_TaxID=4932;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-W303;
 RX MEDLINE=91094833; PubMed=1986220;
 RA Damak F., Boy-Marcotte E., le Roscoet D., Guilbaud R., Jacquot M.;
 RT "SDC25, a CDC25-like gene which contains a RAS-activating domain and
 RT is a dispensable gene of *Saccharomyces cerevisiae*";
 RL Mol. Cell. Biol. 11:202-212(1991).
 RN [2]

RP SEQUENCE OF 668-1253 FROM N.A.

RC STRAIN-0136;
 RX MEDLINE=89306677; PubMed=22545538;

RA Boy-Marcotte E., Danak F., Camonis J., Garreau H., Jacquet M.;
 RT "The C-terminal part of a gene partially homologous to CDC 25 gene
 suppresses the cdc25-5 mutation in *Saccharomyces cerevisiae*.";
 RL Gene 77:21-30(1989).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=90260633; PubMed=2188363;
 RA Crechet J.B., Pouillet P., Mistou M.-Y., Parmeggiani A., Camonis J.,
 RA Boy-Marcotte E., Danak F., Jacquet M.;
 RT "Enhancement of the GDP-GTP exchange of RAS proteins by the carboxyl-
 terminal domain of the SCD25;"
 RL Science 248:866-868(1990).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=91156312; PubMed=2000228;
 RA Rey T., Schweighoffer F., Barlat I., Camonis J., Boy-Marcotte E.,
 RA Guibaud R., Jacquie M., Tocque B.;
 RA "The COOH-domain of the product of the *Saccharomyces cerevisiae* SCD25
 gene elicits activation of p21-ras proteins in mammalian cells.";
 RL Oncogene 6:347-349(1991).
 CC !-- MISCELLANEOUS: SUPPRESSES THE CDC25-5 MUTATION IN YEAST (RESTORES
 CC CAMP LEVEL) AND HAS SIMILAR FUNCTIONS AS CDC25.
 CC !-- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC !-- SIMILARITY: CONTAINS 1 RAS-GEF DOMAIN.
 CC !-- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
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 DR EMBL: M26547; AAA16565.1; --.
 DR PIR: S14177; S14177.
 DR SGD: S0003939; SDC25.
 DR InterPro: IPR000651; RasGEF_N.
 DR InterPro: IPR001895; RasGRF_CDC25.
 DR Pfam: PF00018; SH3; 1.
 DR PROSITE; PS0017; RasGEF; 1.
 DR Pfam: PF00617; RasGEF; 1.
 DR SMART; SMD0229; RasGEF_N; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR KW Guanine nucleotide releasing factor; Cell cycle; Cell division;
 KW SH3 domain.
 FT DOMAIN 26 98 SH3.
 FT DOMAIN 74 79 POLY-ASN.
 FT VARIANT 434 437 POLY-ARG.
 SQ SEQUENCE 1253 AA; 14979 MW; 2DE2C9PC27E3E60D CRC64;

Query Match 55.1%: Score 38; DB 1; Length 180;
 Best Local Similarity 77.8%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY . 1 ALYKKWKKNK 9
 DB 101 ALYKIDWKNN 109

RESULT 15

Y754_MEIJJA ID Y754_MEIJJA STANDARD; PRT; 185 AA.
 AC Q50164;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Hypothetical protein MJ0754.
 GI MJ0754.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.L., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geysen H.G., Fuhrmann J.L., Nguven D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Salow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
 RA Jannaschii;"
 RI Science 273:1058-1073(1996).

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CC

DR EMBL; U67521; AAB98756.1; -.

DR TIGR; MJ0754; -.

KW Hypothetical protein; Complete proteome

SQ SEQUENCE 185 AA; 21765 MW; 2CE5FC9D24895F6 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 185;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKWLKS 13
| | ||| : : |:
Db 38 LYNKWKIQLIFKN 49

Search completed: December 30, 2002, 16:22:28
Job time : 13 secs

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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 30, 2002, 16:20:53 ; Search time 28 Seconds
 (without alignments)
 95.665 Million cell updates/sec

Title: US-09-648-816B-9
 Perfect score: 69
 Sequence: ALYKKWKNKLKS 13

Scoring table: BLOSSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL_21;*

1: sp_archae:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match Length	DB ID	Description
1	47	68	1	508 16 Q8R6X0
2	44	63	8	215 10 Q9Z655
3	44	63	8	827 10 Q04578
4	43	62	3	1891 12 Q8Q024
5	43	62	3	2508 12 Q8Q023
6	42	60	9	293 12 Q67584
7	41	59	4	107 10 Q9L196
8	41	59	4	286 16 Q98PB3
9	41	59	4	307 2 Q9KH70
10	41	59	4	439 12 Q8V8P3
11	41	59	4	531 3 Q74858
12	41	59	4	762 8 Q9G8T2
13	40	58	0	87 16 Q92PK1
14	40	58	0	170 16 Q8YCA3
15	40	58	0	259 2 P72185
16	40	58	0	351 16 Q93IR9

ALIGNMENTS

RESULT 1

ID	PRELIMINARY;	PRT;	508 AA.
Q8R6X0;			
AC			
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Hypothetical protein "TE2663".		
GN	TTR2663.		
OS	Thermoanaerobacter tenaxcongensis.		
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Thermoanaerobacteriaceae; Thermoanaerobacter.		
OX	NCBI-TaxID=119072;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MB4T / JCM1107;		
RX	MEDLINE=2199816; PubMed=11997336;		
RA	Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;		
RA	NCTC-TaxID=119072;		
RA	[1]		
RA	SEQUENCE FROM N.A.		
RA	STRAIN=MB4T / JCM1107;		
RA	MEDLINE=2199816; PubMed=11997336;		
RA	Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;		
RA	NCTC-TaxID=119072;		
RT	"A complete sequence of T. tengcongensis genome.";		
RL	Genome Res. 12:689-700(2002).		
DR	DR: AEG13206; AAM25782.1; -.		
KW	Hypothetical Protein; Complete Proteome.		
SQ	SEQUENCE 508 AA; 58270 MW; BCBB3664EB79D845 CRC64;		

Query Match Best Local Similarity 66.7%; Score 47; DB 16; Length 508; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKS 13

Db 310 LYKAWKEKLUKA 321

RESULT 2

ID	PRELIMINARY;	PRT;	215 AA.
Q9Z655			
AC	Q9Z655;		

DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	ID	Q89024	PRELIMINARY;	PRT;	1891 AA.
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)	AC	Q89024;			
DT	01-JUN-2002 (TREMBLrel. 21, Created)	DR	01-JUN-2002	(TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DR	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
OS	Zymomonas mobilis.	OS				
OC	Bacterium; Proteobacteria; alpha subdivision; Sphingomonadaceae;	OC				
OC	Zymomonas.	NCBI_TAXID=542;				
OX	[1]	SEQUENCE FROM N.A.				
RN		STRAIN=Zm4;				
RA	Um H. W., Kang H.S.;	"Sequence analysis of 43P9 fosmid clone of Zymomonas mobilis Zm4.";				
RA	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.	EMBL: AF02543; AAD19422; 1; .				
KW	Hypothetical protein.	Hypothetical protein.				
SQ	SEQUENCE 215 AA; 25210 MW;	48D3088672D9A05B CRC64;				
Query Match	Best Local Similarity 63.8%; Score 44; DB 2; Length 215;					
Matches	8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
QY	2 LYKKWNKLK 12					
Db	36 LFKSWKAKLK 46					
RESULT 3						
ID	004578	PRELIMINARY;	PRT;	827 AA.		
AC	Q04578					
DT	01-JUL-1997 (TREMBLrel. 04, Created)					
DT	01-JUL-1999 (TREMBLrel. 04, Last sequence update)					
DT	01-JUL-2002 (TREMBLrel. 20, Last annotation update)					
DE	F19K23.6 protein.					
GN	F19K23.6					
OS	Arabidopsis thaliana (Mouse-ear cress).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;					
OC	eurosidic II; Brassicales; Brassicaceae; Arabidopsis.					
OX	NCBI_TAXID=3702;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CV. COLUMBIA;					
RA	Osborne B.I., Vysotskaiia V.S., Toriumi M., Yu G., Oji O., Shen Y.K.,					
RA	Araujo R., Au M., Buehler E., Conway A.R., Dewar K.,					
RA	Feng J., Kim D., Kurtz D., Li Y., Shin P., Sun H., Davis R.W.,					
RA	Ecker J.R., Federici N.A., Theologis A.; Theologis A.;					
RA	"The sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1.,"					
RT	Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.					
RL	[2]					
RN	SEQUENCE FROM N.A.					
RC	STRAIN=CV. COLUMBIA;					
RA	Theologis A.;					
RA	Theologis A.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.					
RL						
DR	EMBL: AAC00375; AAB60760; 1; .					
DR	InterPro: IPR03360; mTERF.					
DR	InterPro: IPR03380; Prantne_attach.					
DR	Pfam: PF02536; mTERF; 2.					
DR	PROSITE: PS00012; PHOSPHOPANTETHINE; UNKNOWN_1.					
DR	SEQUENCE: 827 AA; 92517 MW; 053CB152315555B CRC64;					
Query Match	Best Local Similarity 63.8%; Score 44; DB 10; Length 827;					
Matches	8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;					
QY	1 ALYKKWNKLK 13					
Db	282 AMFKKWPNTIKS 294					
RESULT 4						
QY	1 ALYKKWNKLK 13					
Db	1383 ALYKKWPNSFVDS 1395					
RESULT 5						
QY	1 ALYKKWNKLKS 13					
Db	1383 ALYKKWPNSFVDS 1395					
RESULT 6						
QY	1 ALYKKWNKLKS 13					
Db	1383 ALYKKWPNSFVDS 1395					

067584 PRELIMINARY; PRT; 293 AA.
 ID 067584;
 AC 067584;
 DT 01-NOV-1995 (TREMBLrel. 01, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE B1L protein.
 GN
 OS Bean golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maxwell R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
 RA Maxwell D.P., Russell D.P.;
 RT "Cloning of the complete DNA genomes of four bean-infecting
 geminiviruses and determining their infectivity by electric discharge
 particle acceleration.",
 RL Phytopathology 81:980-985(1991).
 RP [2]
 SEQUENCE FROM N.A.
 RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
 RA Morales F.J., Maxwell D.P.;
 RT "Differentiation of bean infecting geminiviruses by nucleic acid
 hybridization probes and aspects of bean golden mosaic in Brazil.",
 RL Plant Dis. 75:336-342(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
 RT "Genetic diversity in geminiviruses causing bean golden mosaic
 disease: the nucleotide sequence of the infectious cloned DNA
 components of a Brazilian isolate of bean golden mosaic geminivirus.",
 RL Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
 DR M8867; RAA46317.1; --.
 DR Interpro; IPR000211; Gemini BLI.
 DR Pfam; PF00845; Gemini_BLI; 1.
 SQ SEQUENCE 293 AA; 33049 MW; FEE2D535B3984854 CRC64;
 Query Match 60 9%; Score 42; DB 12; Length 293;
 Best Local Similarity 63.6%; Pred. No. 54;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 YKKWKWKLKS 13
 | ||| |||||
 Db 178 YGKWERKLKS 188
 RESULT 7
 ID Q9L196
 PRELIMINARY; PRT; 107 AA.
 AC 09L196;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE Genomic DNA, chromosome 3, Platclone:MO10.
 OS Arabidopsis thaliana (Mouse ear cress).
 OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
 OC Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RP [1]
 SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 MEDLINE=20363099; PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
 RT TAC and BAC clones.", 1.
 RP
 RL DNA Res. 7:217-221(2000).
 ID DR EMBL; AP001309; BAB02553.1; -.
 SQ SEQUENCE 107 AA; 12145 MW; 020D0D5842B14BC CRC64;
 Query Match 59.4%; Score 41; DB 10; Length 107;
 Best Local Similarity 65.7%; Pred. No. 29;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 YKKWKWKLKS 11
 | ||| |||||:
 Db 96 HKKWKWNKV 104
 RP RESULT 8
 ID Q98PE3
 PRELIMINARY; PRT; 286 AA.
 AC 098PE3;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE Hypothetical protein MYPU_7800.
 GN MYPU_7800.
 OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Bacillus/clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAB CTPP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chambaud I., Heilig R., Farris S., Barbe V., Samson D., Galisson F.,
 RA Mozer L., Byvbig K., Wroblewski H., Viari A., Rocha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis.",
 RL Nucleic Acids Res. 29:2145-2153(2001).
 DR EMBL; AL44566; CAC13953.1; -.
 DR MyPubList; MP0U_7800; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 286 AA; 34833 MW; 17B4F37548A9C081 CRC64;
 Query Match 59.4%; Score 41; DB 16; Length 286;
 Best Local Similarity 54.5%; Pred. No. 76;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LYKKWKWKLK 12
 | ||| |||||:
 Db 137 IHYWKWNILK 147
 RP
 RESULT 9
 ID Q9KH70
 PRELIMINARY; PRT; 307 AA.
 AC Q9KH70;
 Q9KH70;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Thermostable dipeptidase Bbp.
 GN Bbp.
 OS Brevibacillus borstelensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Paenibacillaceae; Brevibacillaceae.
 OX NCBI_TaxID=45462;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCCS-1;
 RA Kwon S., Hong S., Sung M.;
 RT "A Novel Thermostable Dipeptidase from Brevibacillus borstelensis BCCS-
 1.",
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 DR AF26476; AAF97793.1; -.
 DR Interpro; IPR000180; Renal_dipeptidase.
 PRAM; PF01244; Renal_dipeptidase; 1.

[1] RN
 R P
 SEQUENCE FROM N. A.
 STRAIN-CLIP 11262 / SEROVAR 6A;
 RC
 PubMed=11679569;
 RA
 Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
 Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 Domann E., Dominguez-Bernal G., Dubchaud E., Durant L., Dussurget O.,
 Entian K.-D., Fischi H., Garcia-del Portillo F., Garrido P.,
 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaeprt U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
 Madueno E., Maitouran A., Mata Vicente J., Ng E., Nedari H.,
 Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 Vazquez-Boland J.-A., Voss H., Wenzel J., Cossart P.;
 RT
 "Comparative genomics of Listeria species.";
 RL
 Science 294: 849-852(2001);
 EMBL; AL59616; CAC95336; 1; -;
 DR
 ListList; LIN60103; -;
 KW
 Hypothetical protein; Complete proteome;
 SQ
 SEQUENCE 87 AA; 10135 MW; E1A37A29CAC6E4DF CRC64;

Query Match 58.0%; Score 40; DB 16; Length 87;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 YKKWKNK 9
 ||||:|||
 Db 77 YKKWENK 83

RESULT 14
 08YGA3 PRELIMINARY; PRT; 170 AA.
 AC 08YGA3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE DIBN protein.
 OS Brucellaceae.
 OC
 Bacterium; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 Brucellaceae; Brucellaceae.
 OX NCBI-TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC
 08YGA3 PRELIMINARY; PRT; 170 AA.
 AC 08YGA3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE DIBN protein.
 OS Brucellaceae.
 OC
 Bacterium; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 Brucellaceae; Brucellaceae.
 OX NCBI-TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC
 08YGA3 PRELIMINARY; PRT; 170 AA.
 AC 08YGA3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE DIBN protein.
 OS Brucellaceae.
 OC
 Bacterium; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 Brucellaceae; Brucellaceae.
 OX NCBI-TaxID=29459;

Query Match 58.0%; Score 40; DB 16; Length 170;
 Best Local Similarity 63.6%; Pred. No. 66; Length 170;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ALYKKWKNKL 11
 || :|||:|||
 Db 9 AYVNNQWANKL 19

[1] DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE Repressor protein (HEMR protein).
 GN HEMR.
 OS Propionibacterium freudenreichii.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Propionibacteriales; Propionibacteriaceae;
 OC Propionibacterium.
 OX NCBI-TaxID=1744;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA Roessner C.A.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 17-259 FROM N. A.
 RC STRAIN=TFO12424;
 RX MEDLINE=9317878; PubMed=8439165;
 RA Murakami K., Hashimoto Y., Murooka Y.;
 RT "Cloning and characterization of the gene encoding glutamate 1-semialdehyde 2,1-aminomutase, which is involved in delta-aminolevulinic acid synthesis in Propionibacterium freudenreichii.";
 RL Appl. Environ. Microbiol. 59:347-350(1993).
 RN [3]
 RP SEQUENCE OF 17-259 FROM N. A.
 RC STRAIN=TFO12424;
 RA Hashimoto Y., Yamashita Y., Ono H., Murooka Y.;
 RT J. Ferment. Bioeng. 82:93-100(1996).
 RL J. Ferment. Bioeng. 82:93-100(1996).
 RN [4]
 RP SEQUENCE OF 17-259 FROM N. A.
 RC STRAIN=TFO12424;
 RX MEDLINE=97306686; PubMed=9163953;
 RA Hashimoto Y., Yamashita Y., Murooka Y.;
 RT "The Propionibacterium freudenreichii hemHXBRL gene cluster, which encodes enzymes and a regulator involved in the biosynthetic pathway from glutamate to procheme.";
 RT RL Appl. Microbiol. Biotechnol. 47:385-392(1997).
 CC CCAU-1 SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS.
 DR EMBL; U51164; ARB07865; 1; -;
 DR EMBL; D85417; BA221913; 1; -;
 DR InterPro; IPR001647; HTH_Tetr.
 DR Pfam; PF00440; tetr; 1.
 DR Pfam; PF00440; tetr; 1.
 KW DNA-binding; transcription regulation.
 SQ SEQUENCE 259 AA; 27426 MW; 5FCB0EF342606170 CRC64;

Query Match 58.0%; Score 40; DB 2; Length 259;
 Best Local Similarity 66.7%; Pred. No. 99; Length 259;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ALYKKWKNK 9
 ||||:|||
 Db 76 ALYRRWNK 84

Search completed December 30, 2002, 16:23:05
 Job time : 31 secs

RESULT 15
 PT2185 PRELIMINARY; PRT; 259 AA.
 ID P72185; PRELIMINARY; PRT; 259 AA.
 AC P72185;

